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ANT1m ATGGGTGATCACGCTTGGAGTTCTAAAGGACTTCCTGGCCGGGGCGGTGCGCGTGCGCTCTCCAAGACGCGGTGCG 80
ANT2m ATGAGAGATGCGCGTGTGTCCTTCGCCAAGGACTTCCTGGCAGGTGGAGTGGCCGAGCCATCTCCAAGACGCGGTAGC 80
ANT3m ATGAGGGAACAGGCCATCTCCTTCGCCAAAGACTTCTGGCCGAGGCAATCGCCGCGCCATCTCCAAGACGCGGTGCG 80

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ANT3m TCCGATCGAGCGGGTCAAGCTGCTGCTGCAGGTCCAGCATGCCAGCAAGCAGATCGCGCGACAAGCAGTACAAAGGGA 160

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ANT3m TCGTGGACTGCATTTGTCGGATCCCAAGGAGCAGGGCGTGTCTCTCTTGAGGGGTAACTGGCCAACGTGATCCGT 240

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ANT3m CCGGGCGGCTACTTCGGGTGTAGATACGGCAAGGGATGCTCCCGACCCCAAGAACACGCACATCGTGTGAGCT 640

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ANT3m GGATGATCGGACAGACGTGACGGCGTGGCGGGCTGTGTCTACCCCTTGACACGGTGGCGGGCGCATGATGATG 720

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ANT2m CAGTCAAGGGCGAAAGGAAGTACATCATGTACACAGGCAAGTTGACTGCTGGCGGAAGATTGCTGCTGATGAAGGAGG 800
ANT3m CAGTCCGGGCGAAAGGAGCTGACATCATGTACACGGGCAAGTTGACTGTTGGAGGAAGATCTTCAAGATGAGGGGG 800

| | | |
|-------|---|-----|
| ANT1m | CAAGGCCTTCTTCAAAAGGTGCTGGTCCAATGTCTGAGAGGCATGGGCGGTGCTTTTGTATTTGGTGTGTATGATGAGA | 877 |
| ANT2m | CAAAGCTTTTCAAGGGTGCAATGGTCCAATGTCTCAGAGGCATGGGCGGTGCTTTTGTGCTTGTCTTGTATGATGAAA | 880 |
| ANT3m | CAAGGCCTTCTTCAAGGGTGCTGGTCCAACGTCCTGGGGGCATGGGGGGCGCTTCGTGCTGGTCCTGTACGACGAGC | 880 |
| ANT1m | TCAAAAATATGTCTAA | 894 |
| ANT2m | TCAAGAAGTACACATAA | 897 |
| ANT3m | TCAAGAAGGTGATCTAA | 897 |

Fig. 1B

| | | |
|--------|--|-----|
| hANT1p | MGDHAWSFLKDFLAGAVAAVSKTAVAPIERVKLLLQVQHASKQISAEKQ | 50 |
| hANT2p | MTDAAVSFAKDFLAGGVAAATSKTAVAPIERVKLLLQVQHASKQITADKQ | 50 |
| hANT3p | MTEQAISFAKDFLAGGIAAATSKTAVAPIERVKLLLQVQHASKQIAADKQ | 50 |
| hANT1p | YKGIIDCVVRIPKEQGLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFL | 100 |
| hANT2p | YKGIIDCVVRIPKEQGLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFL | 100 |
| hANT3p | YKGIIDCVVRIPKEQGLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFL | 100 |
| hANT1p | GGVDRHKQFWRYFAGNLASGGAAGATSLCFVYPLDFARTRLAADVGRRA | 149 |
| hANT2p | GGVDKRTQFWRYFAGNLASGGAAGATSLCFVYPLDFARTRLAADVKGAGA | 150 |
| hANT3p | GGVDKHTQFWRYFAGNLASGGAAGATSLCFVYPLDFARTRLAADVKGSGT | 150 |
| hANT1p | QREFHGLGDCIKIKFSDGIRGLYQGFNVSVQGIIYRAAYFGVYDTAKG | 199 |
| hANT2p | EREFRGLGDCIKIKFSDGIRGLYQGFNVSVQGIIYRAAYFGVYDTAKG | 200 |
| hANT3p | EREFRGLGDCIKIKFSDGIRGLYQGFNVSVQGIIYRAAYFGVYDTAKG | 200 |
| hANT1p | MLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMMQSGRKGADIM | 249 |
| hANT2p | MLPDPKNTHIVISWMIAQTVTAVAGLLSYPFDTVRRRMMMQSGRKGADIM | 250 |
| hANT3p | MLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMMQSGRKGADIM | 250 |
| hANT1p | YTGTVDCWRKIAKDEGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV. | 298 |
| hANT2p | YTGTDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYT. | 299 |
| hANT3p | YTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKVI. | 299 |

Fig. 2

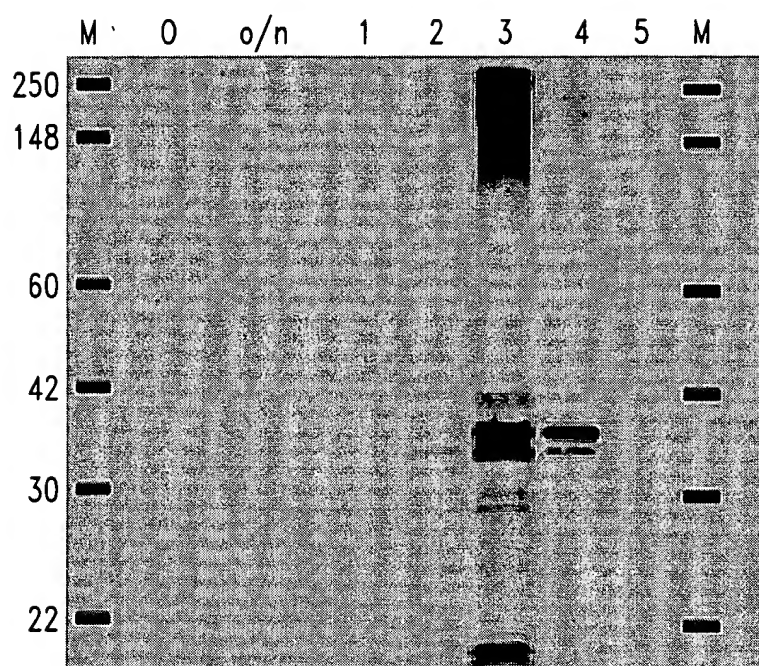


Fig. 3

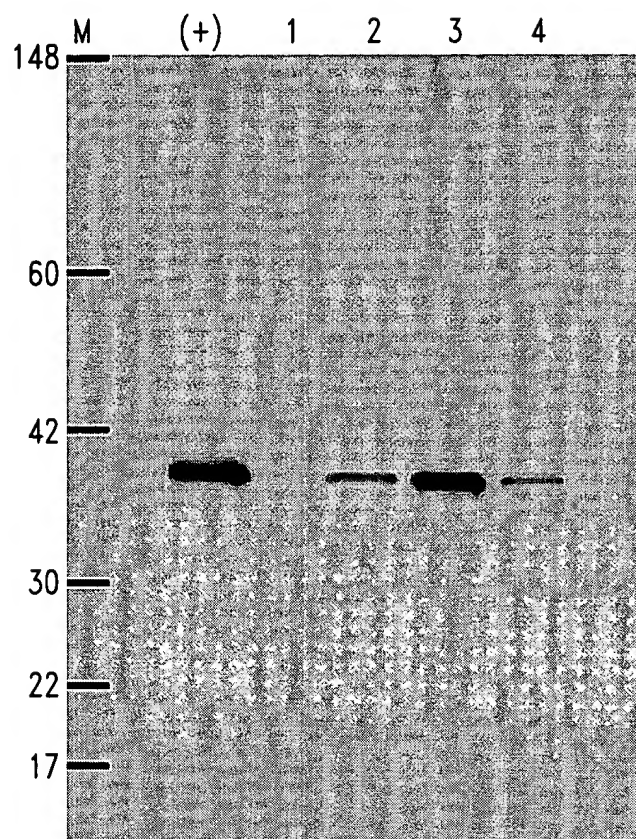


Fig. 4

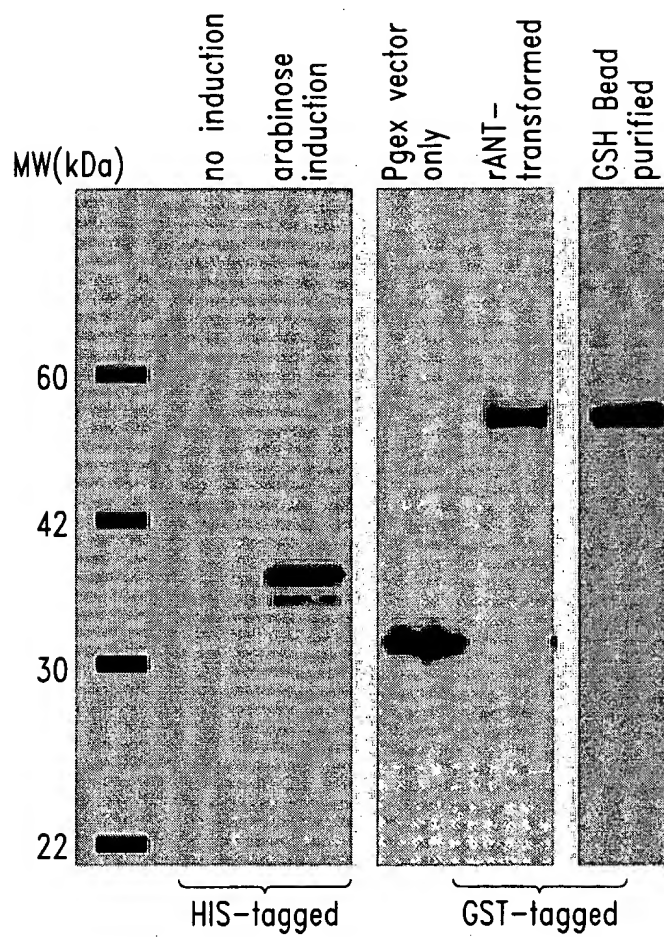


Fig. 5

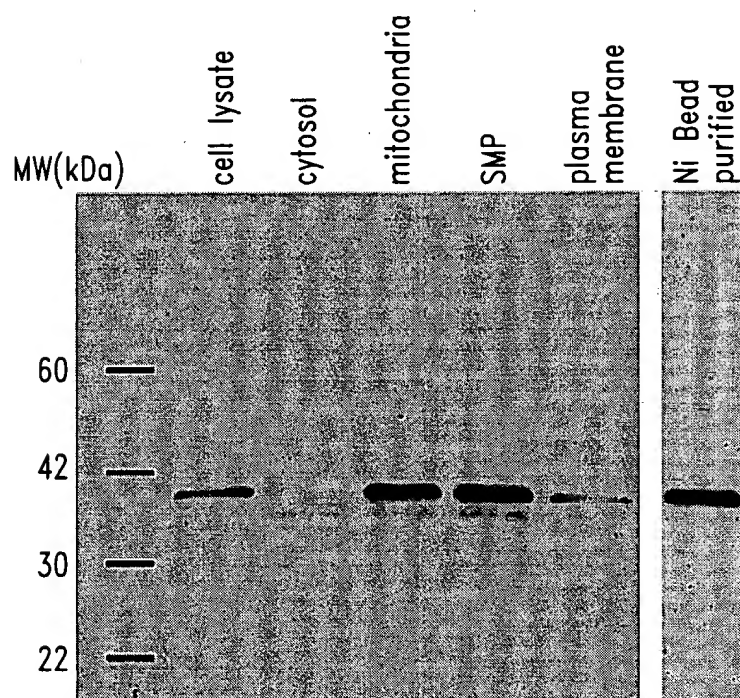


Fig. 6

ATGGTCAACCCACCGTGTTCTTCGACATTGCCGTCGACGGCGAGCCCTTGGGCCGCGTCTCCTTTGAGC 70
TACCAGTTGGGGTGGCACAAGAAGCTGTAACGGCAGCTGCCGCTCGGGAACCCGGCGCAGAGGAACTCG
M V N P T V F F D I A V D G E P L G R V S F E

TGTTTGCAGACAAGGTCCCAAAGACAGCAGAAAAATTTTCGTGCTCTGAGCACTGGAGAGAAAGGATTTGG 140
ACAAACGTCTGTTCCAGGGTTTCTGTCGTCTTTTAAAAGCACGAGACTCGTGACCTCTCTTTCCTAAACC
L F A D K V P K T A E N F R A L S T G E K G F G

TTATAAGGGTTCCTGCTTTACAGAATTATTCAGGGTTTATGTGTCAGGGTGGTGACTTCACACGCCAT 210
AATATTCCCAAGGACGAAAGTGCTTAATAAGGTCCCAAATACACAGTCCCACCACTGAAGTGTGCGGTA
Y K G S C F H R I I P G F M C Q G G D F T R H

AATGGCACTGGTGGCAAGTCCATCTATGGGGAGAAATTTGAAGATGAGAACTTCATCCTAAAGCATACGG 280
TTACCGTGACCACCGTTTCAGGTAGATACCCCTCTTTAAACTTCTACTCTTGAAGTAGGATTTTCGTATGCC
N G T G G K S I Y G E K F E D E N F I L K H T

GTCCTGGCATCTTGTCCATGGCAAATGCTGGACCCAACACAAATGGTTCACAGTTTTTCATCTGCACTGC 350
CAGGACCGTAGAACAGGTACCGTTTACGACCTGGGTTGTGTTTACCAAGGGTCAAAAAGTAGACGTGACG
G P G I L S M A N A G P N T N G S Q F F I C T A

CAAGACTGAGTGGTTGGATGGCAAGCATGTGGTGTGGCAAAGTGAAAGAAGGCATGAATATTGTGGAG 420
GTTCTGACTACCAACCTACCGTTTCGTACACCACAAACCGTTTCACCTTCTCCGTACTTATAACACCTC
K T E W L D G K H V V F G K V K E G M N I V E

GCCATGGAGCGCTTTGGGTCCAGGAATGGCAAGACCAGCAAGAAGATCACCATTGCTGACTGTGGACAAC 490
CGGTACCTCGCAAACCCAGGTCTTACCGTTCTGGTCGTTCTTCTAGTGGTAACGACTGACACCTGTTG
A M E R F G S R N G K T S K K I T I A D C G Q
TCGAATAA 498
AGCTTATT
L E .

Fig. 7

ATGGTCAACCCACCGTGTTCTTCGACATTGCCGTCGACGGCGAGCCCTTGGGCGCGTCTCCTTTGAGC 70
TACCAGTTGGGGTGGCACAAGAAGCTGTAACGGCAGCTGCCGCTCGGGAACCCGGCGCAGAGGAACTCG
M V N P T V F F D I A V D G E P L G R V S F E

TGTTTGCAGACAAGGTCCCAAAGACAGCAGAAAATTTTCGTGCTCTGAGCACTGGAGAGAAAGGATTTGG 140
ACAAACGTCTGTTCCAGGGTTTCTGTCGTCTTTTAAAAGCACGAGACTCGTGACCTCTCTTTCCTAAACC
L F A D K V P K T A E N F R A L S T G E K G F G

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AATATTCCCAAGGACGAAAGTGTCTTAATAAGGTCCCAAATACACAGTCCCACCACTGAAGTGTGCGGTA
Y K G S C F H R I I P G F M C Q G G D F T R H

AATGGCACTGGTGGCAAGTCCATCTATGGGGAGAAATTTGAAGATGAGAACTTCATCCTAAAGCATACGG 280
TTACCGTGACCACCGTTCAGGTAGATACCCCTCTTTAAACTTCTACTCTTGAAGTAGGATTTTCGTATGCC
N G T G G K S I Y G E K F E D E N F I L K H T

GTCCTGGCATCTTGTCCATGGCAAATGCTGGACCCAACACAAATGGTCCCAGTTTTTCATCTGCACTGC 350
CAGGACCGTAGAACAGGTACCGTTTACGACCTGGGTTGTGTTTACCAAGGGTCAAAAAGTAGACGTGACG
G P G I L S M A N A G P N T N G S Q F F I C T A

CAAGACTGAGTGGTTGGATGGCAAGCATGTGGTGTGGCAAAGTGAAAGAAGGCATGAATATTGTGGAG 420
GTTCTGACTACCAACCTACCGTTCGTACACCACAAACCGTTTCACCTTCTTCCGTACTTATAACACCTC
K T E W L D G K H V V F G K V K E G M N I V E

GCCATGGAGCGCTTTGGGTCCAGGAATGGCAAGACCAGCAAGAAGATCACCATTGCTGACTGTGGACAAC 490
CGGTACCTCGCAAACCCAGGTCTTACCGTTCGTGGTCTTCTAGTGGTAACGACTGACACCTGTTG
A M E R F G S R N G K T S K K I T I A D C G Q
TCGAATAA 498
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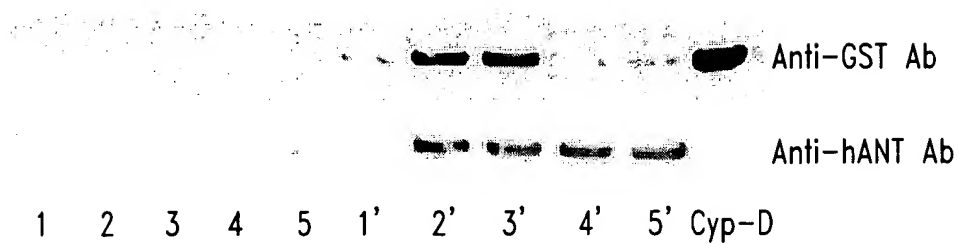


Fig. 9

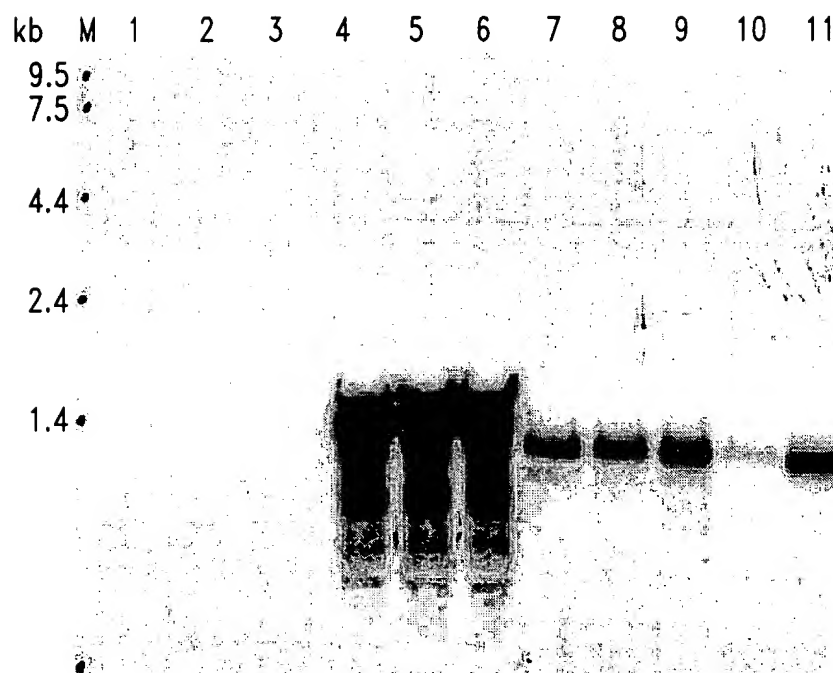


Fig. 10

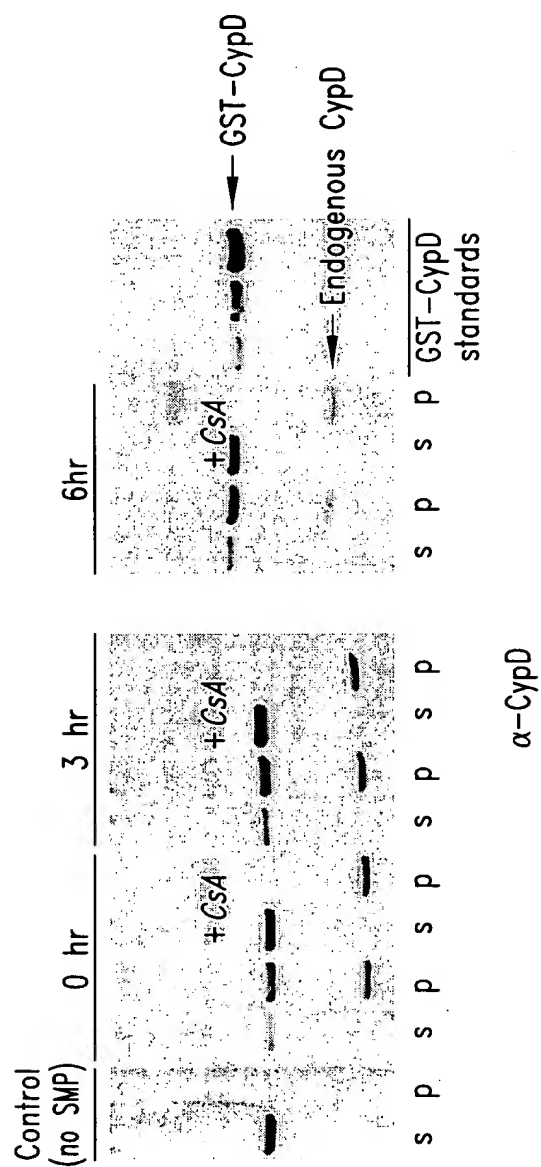


Fig. 11

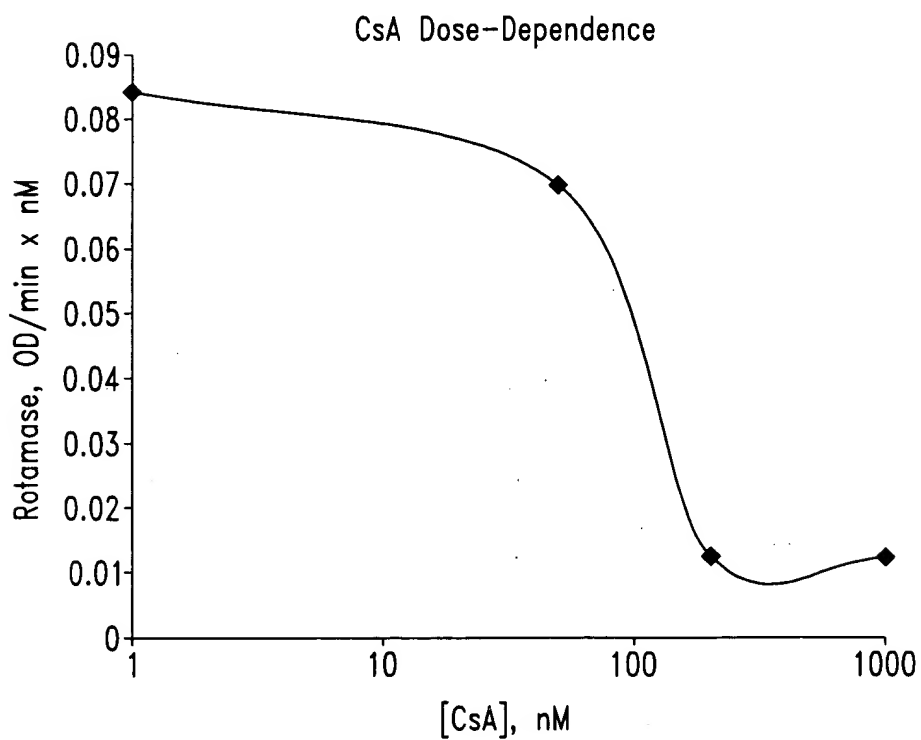
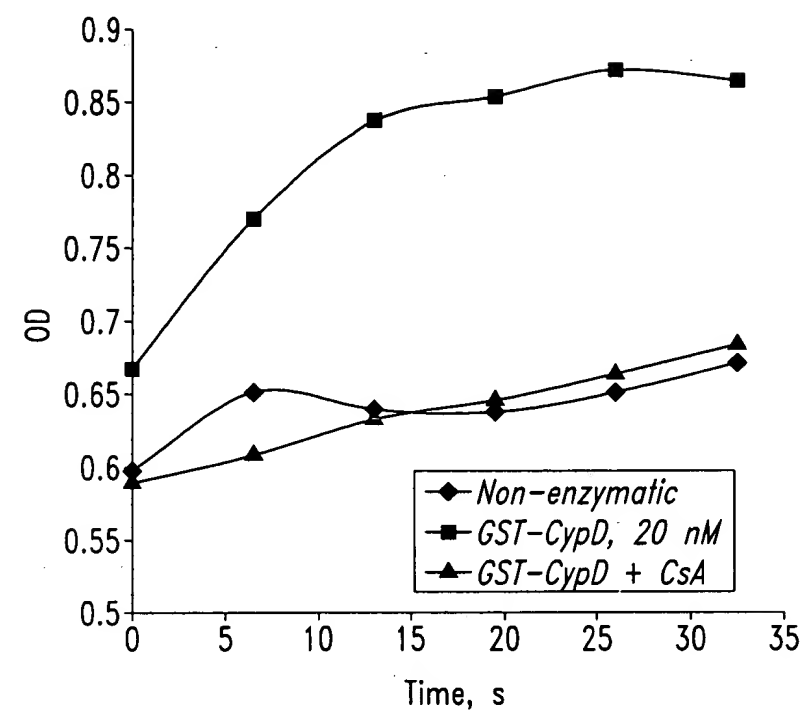


Fig. 12

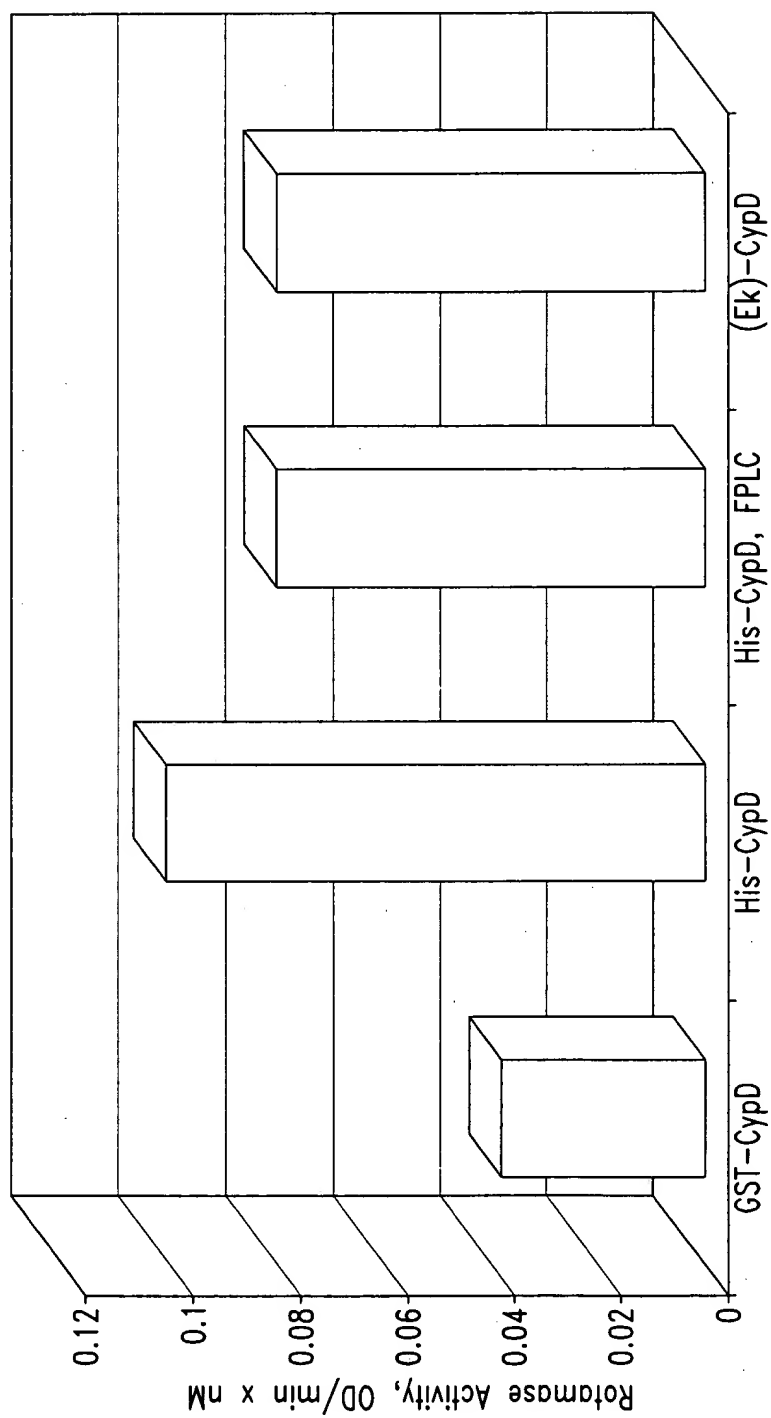


Fig. 13

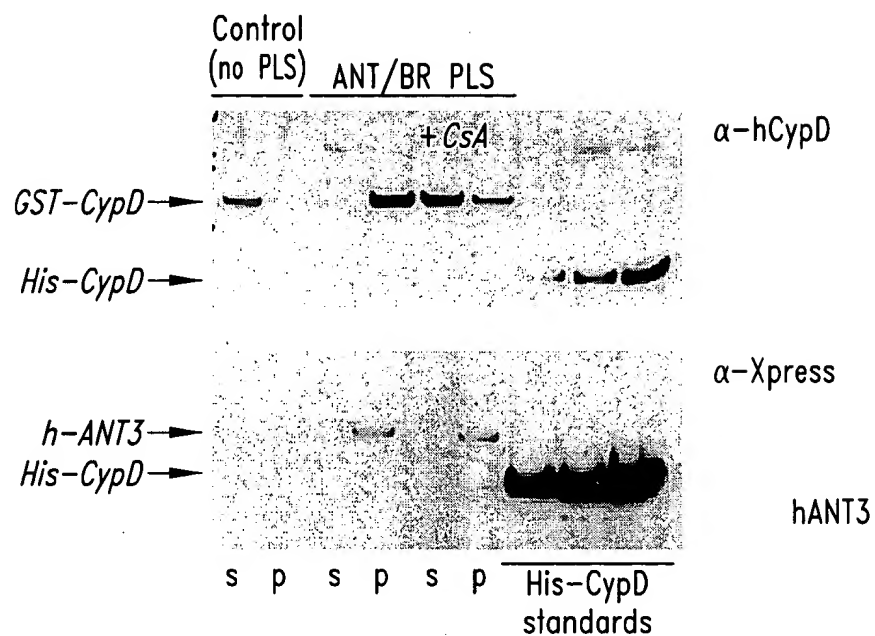


Fig. 14

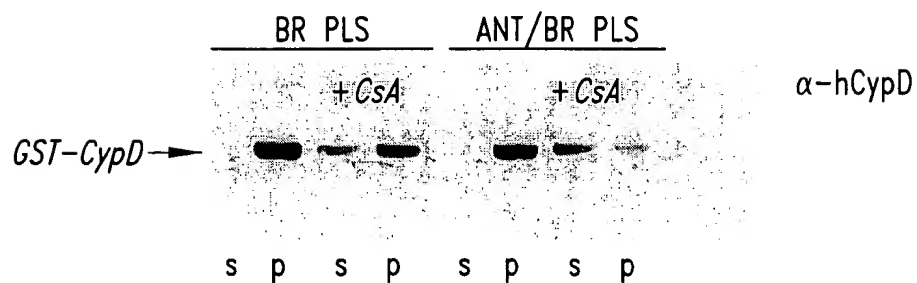


Fig. 15